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## RAW SEQUENCE LISTING

DATE: 11/09/2001

PATENT APPLICATION: US/09/875,221A

TIME: 15:52:35

Input Set : A:\Carp0089.ST25.txt

Output Set: N:\CRF3\11092001\I875221A.raw

3 <110> APPLICANT: Athwal, Diljeet Singh  
 4 Brown, Derek Thomas  
 5 Weir, Andrew Neil Charles  
 6 Popplewell, Andrew George  
 7 Chapman, Andrew Paul  
 8 King, David John  
 10 <120> TITLE OF INVENTION: Biological Products  
 12 <130> FILE REFERENCE: Carp-0089  
 14 <140> CURRENT APPLICATION NUMBER: 09/875,221A  
 15 <141> CURRENT FILING DATE: 2001-06-06  
 17 <150> PRIOR APPLICATION NUMBER: GB0013810.7  
 18 <151> PRIOR FILING DATE: 2000-06-06  
 20 <160> NUMBER OF SEQ ID NOS: 130  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 5  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Artificial Sequence *OK*  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: hTNF40 CDRH1  
 32 <400> SEQUENCE: 1  
 34 Asp Tyr Gly Met Asn  
 35 1 5  
 38 <210> SEQ ID NO: 2  
 39 <211> LENGTH: 17  
 40 <212> TYPE: PRT  
 41 <213> ORGANISM: Artificial Sequence *OK*  
 43 <220> FEATURE:  
 44 <223> OTHER INFORMATION: hTNF40/human hybrid CDRH2  
 46 <400> SEQUENCE: 2  
 48 Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys  
 49 1 5 10 15  
 52 Gly  
 56 <210> SEQ ID NO: 3  
 57 <211> LENGTH: 9  
 58 <212> TYPE: PRT  
 59 <213> ORGANISM: Artificial Sequence *OK*  
 61 <220> FEATURE:  
 62 <223> OTHER INFORMATION: hTNF40 CDRH3  
 64 <400> SEQUENCE: 3  
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 67 1 5  
 70 <210> SEQ ID NO: 4  
 71 <211> LENGTH: 11  
 72 <212> TYPE: PRT  
 73 <213> ORGANISM: Artificial Sequence  
 75 <220> FEATURE:

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76 <223> OTHER INFORMATION: hTNF40 CDRL1
78 <400> SEQUENCE: 4
80 Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
81 1          5          10
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85 <211> LENGTH: 7
86 <212> TYPE: PRT
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
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92 <400> SEQUENCE: 5
94 Ser Ala Ser Phe Leu Tyr Ser
95 1          5
98 <210> SEQ ID NO: 6
99 <211> LENGTH: 9
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: hTNF40 CDRL3 /
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108 Gln Gln Tyr Asn Ile Tyr Pro Leu Thr
109 1          5
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 17
114 <212> TYPE: PRT
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: hTNF40 CDRH2 /
120 <400> SEQUENCE: 7
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123 1          5          10          15
126 Gly
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131 <211> LENGTH: 321
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
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136 <223> OTHER INFORMATION: hTF40-gL1 /
138 <220> FEATURE:
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140 <222> LOCATION: (1)..(321)
141 <223> OTHER INFORMATION:
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145 gac att caa atg acc cag agc cca tcc agc ctg agc gca tct gta gga      48
146 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
147 1          5          10          15
149 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac      96
150 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
151          20          25          30

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153 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc      144
154 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
155      35      40      45
157 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga      192
158 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
159      50      55      60
161 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca      240
162 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
163 65      70      75      80
165 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc      288
166 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
167      85      90      95
169 aca ttc ggt cag ggt act aaa gta gaa atc aaa      321
170 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
171      100      105
174 <210> SEQ ID NO: 9
175 <211> LENGTH: 107
176 <212> TYPE: PRT
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: hTF40-gL1
182 <400> SEQUENCE: 9
184 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
185 1      5      10      15
188 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
189      20      25      30
192 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
193      35      40      45
196 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
197      50      55      60
200 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
201 65      70      75      80
204 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
205      85      90      95
208 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
209      100      105
212 <210> SEQ ID NO: 10
213 <211> LENGTH: 321
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
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220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (1)..(321)
223 <223> OTHER INFORMATION:
226 <400> SEQUENCE: 10
227 gac att caa atg acc cag agc cca tcc agc ctg agc gca tct gta gga      48
228 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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229 1          5          10          15
231 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac      96
232 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
233          20          25          30
235 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa ctc ctc atc      144
236 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
237          35          40          45
239 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga      192
240 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
241          50          55          60
243 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca      240
244 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
245 65          70          75          80
247 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc      288
248 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
249          85          90          95
251 aca ttc ggt cag ggt act aaa gta gaa atc aaa      321
252 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
253          100          105
256 <210> SEQ ID NO: 11
257 <211> LENGTH: 107
258 <212> TYPE: PRT
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: hNF40-gL2
264 <400> SEQUENCE: 11
266 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
267 1          5          10          15
270 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
271          20          25          30
274 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
275          35          40          45
278 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
279          50          55          60
282 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
283 65          70          75          80
286 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
287          85          90          95
290 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
291          100          105
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295 <211> LENGTH: 354
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: ghlhTNF40.4 (Figure 10)
302 <220> FEATURE:
303 <221> NAME/KEY: CDS
304 <222> LOCATION: (1)..(354)

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305 &lt;223&gt; OTHER INFORMATION:

308 &lt;400&gt; SEQUENCE: 12

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309 cag gtg cag ctg gtc cag tca gga gca gag, gtt aag aag cct ggt gct      48
310 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
311 1          5          10          15
313 tcc gtc aaa gtt tgc tgt aag gcc tca ggc tac gtg ttc aca gac tat      96
314 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
315          20          25          30
317 ggt atg aat tgg gtc aga cag gcc ccg gga caa ggc ctg gaa tgg atg      144
318 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
319          35          40          45
321 ggt tgg att aat act tac att gga gag cct att tat gct caa aag ttc      192
322 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
323          50          55          60
325 cag ggc aga gtc acg ttc act cta gac acc tcc aca agc act gca tac      240
326 Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
327 65          70          75          80
329 atg gag ctg tca tct ctg aga tcc gag gac acc gca gtg tac tat tgt      288
330 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
331          85          90          95
333 gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc      336
334 Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
335          100          105          110
337 cta gtc aca gtc tcc tca      354
338 Leu Val Thr Val Ser Ser
339          115

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342 &lt;210&gt; SEQ ID NO: 13

343 &lt;211&gt; LENGTH: 118

344 &lt;212&gt; TYPE: PRT

345 &lt;213&gt; ORGANISM: Artificial Sequence

347 &lt;220&gt; FEATURE:

348 &lt;223&gt; OTHER INFORMATION: ghlhTNF40.4 (Figure 10)

350 &lt;400&gt; SEQUENCE: 13

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352 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
353 1          5          10          15
356 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
357          20          25          30
360 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
361          35          40          45
364 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe
365          50          55          60
368 Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr
369 65          70          75          80
372 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
373          85          90          95
376 Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
377          100          105          110
380 Leu Val Thr Val Ser Ser
381          115

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VERIFICATION SUMMARY

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